

REMARKS

Applicants believe no new matter is added by this amendment.

Status and amendments to the claims.

In order to expedite prosecution and advance this case toward allowance, the claims have been amended in response to the Office action of August 20, 2008, and this amendment should not be interpreted as acquiescence in the rejection. This amendment is being made in response to the pending Office action, and was not made previously for that reason.

Claims 22, 24-33, 36-38, and 41-44 remain pending. Claims 22, 25-27, 30, 32, 36-38, and 41 are currently amended.

The Examiner has determined that Claim 43 is allowable; Applicants agree with this assessment, and thank the Examiner for his consideration. Applicants note that since claim 44 depends from Claim 43 and further limits the subject matter, Applicants believe that claim 44 should also be allowable.

Support for 60% or 90% identity to the claimed polypeptide may be found in the specification at, for example, page 36, line 32 through page 37, line 2.

Support for greater tolerance to drought conditions may be found, for example, on page 1, line 31, on page 66, line 25, on page 93 at line 11, or on page 95 at line 12.

Response to specific rejections.

Items 7-8. Rejection under 35 USC 112, first paragraph, written description.

Claim 25 has been amended to limit the subject matter of the claim to a transcription factor polypeptide that is at least 90% identical to SEQ ID NO: 14, thus limiting the subject matter of the claim 22. Support for 90% identity is indicated above.

Accordingly, Applicants believe that the present rejection of claim 25, has been avoided by the amendment of the claim.

Item 9. Rejection under 35 USC 112, first paragraph, written description

Applicants believe the amendment of claims 22, 25, 27, 30, 32, 36, 37, 38, and 41 avoids the present rejection.

The present claims are directed to recombinant constructs, and transgenic plants comprising recombinant polynucleotides, where the constructs or polynucleotides encode an AT hook transcription

factor polypeptide. The subject matter is limited by hybridization to the DNA sequences under highly stringent conditions, and the subject matter is further limited by a specific percent identity to the polypeptide. The specification discloses a significant number of phylogenetically related sequence species that have conserved structure, the specification teaches how to identify other related sequence species using hybridization and percent identity, and the specification discloses how claimed sequences have conserved function related to the presence of two conserved domains, that is, structural elements, found within the sequences. These sequences include, for example, soy G3456 (SEQ ID NO: 14) and *Arabidopsis* G2153 (SEQ ID NO: 6). The specification predicts that "equivalogs of these sequences would function in a similar capacity" (page 39, line 31). The specification discloses rice G3401 (SEQ ID NO: 38), listed as an ortholog in Table 5 on page 76.

Furthermore, the previously-submitted declaration of Dr. Ratcliffe shows that all of these sequences conferred increased tolerance to drought. The specification discloses how G3456 (page 95, line 6) and G2153 (page 92, lines 24-26) confer increased biomass. G3401 also confers increased biomass (see U.S. patent application 12/077,535, filed 03-17-2008, page 167, the "G3401", rows showing "More tol. to drought* and better recovery from drought treatment" and "Larger leaf size").

The claimed sequences should include G3456, G2153, and G3401 (see percent identity analysis presented below). Thus, the specification discloses three sequences that relate to the claimed subject matter and functions. As these sequences are derived from very diverse species, they represent a considerable sampling of higher plants. The USPTO, in its 1998 "Request for Comments on Interim Guidelines for Examination of Patent Applications Under the 35 U.S.C. 112 "Written Description" Requirement:

A "representative number of species" requires that the species which are expressly described be representative of the entire genus. Thus, when there is substantial variation within the genus, it may require a description of the various species which reflect the variation within the genus. For example, a broadly drawn claim to a specific gene from ruminant mammals may require a representative species from cattle, buffalo, bison, goat, deer, antelope, camel, giraffe and llama." As the level of expertise in the art has improved considerably since 1998, and since Applicants have provided functionally and structurally-related sequences from very diverse plant species, Applicants believe that they have met the written description requirements.

Accordingly, Applicants believe that the present rejection under 35 USC 112, first paragraph, for lack of written description, has been avoided by the amendment of the claim.

Items 12 and 12. Rejection under 35 USC 102/103 or 103

Applicants believe the amendment of claims 22, 25, 27, 30, 32, 36, 37, 38, and 41 avoids the present rejection.

An Accelrys-based comparison of the full-length sequences of G3456 (SEQ ID NO: 14) and G2153 (SEQ ID NO: 6) shows that the sequences share 65.6% identity:

Comparison of G3456 and G2153

Pairwise Matrix: GONNET
Align Speed: Slow
Open Gap Penalty: 10.000
Extended Gap Penalty: .100
Multiple Matrix: GONNET
Multiple Open Gap Penalty: 10.000
Multiple Extended Gap Penalty: .05
Delay Divergent: 30
Gap Separation Distance: 8
End Gap Separation: false
Residue Specific Penalties: false
Hydrophilic Penalties: false
Hydrophilic Residues: GPSNDQEK
Alignment Score 974
Percent Identity Matrix

	G3456	G2153
G3456	100.0	65.6
G2153	65.6	100.0

A similar analysis between G3456 and G3401 (SEQ ID NO: 38) shows that these sequences share

Comparison of G3456 and G3401

Pairwise Matrix: GONNET
Align Speed: Slow
Open Gap Penalty: 10.000
Extended Gap Penalty: .100
Multiple Matrix: GONNET
Multiple Open Gap Penalty: 10.000
Multiple Extended Gap Penalty: .05
Delay Divergent: 30
Gap Separation Distance: 8
End Gap Separation: false
Residue Specific Penalties: false
Hydrophilic Penalties: false
Hydrophilic Residues: GPSNDQEK
Alignment Score 880

Percent Identity Matrix

	G3456	G3401
G3456	100.0	60.3
G3401	60.3	100.0

However, Accelrys analyses of Bevan's C71448 and Wiegel's sequence show percentage identities of 52.8 and 52.3:

Comparison of G3456 and Bevan's C71448

Pairwise Matrix: GONNET
Align Speed: Slow
Open Gap Penalty: 10.000
Extended Gap Penalty: .100
Multiple Matrix: GONNET
Multiple Open Gap Penalty: 10.000
Multiple Extended Gap Penalty: .05
Delay Divergent: 30
Gap Separation Distance: 8
End Gap Separation: false
Residue Specific Penalties: false
Hydrophilic Penalties: false
Hydrophilic Residues: GPSNDQEKR
Alignment Score 823
Percent Identity Matrix

	G3456	G1076
G3456	100.0	52.8
G1076	52.8	100.0

Comparison of G3456 and Weigel sequence

Pairwise Matrix: GONNET
Align Speed: Slow
Open Gap Penalty: 10.000
Extended Gap Penalty: .100
Multiple Matrix: GONNET
Multiple Open Gap Penalty: 10.000
Multiple Extended Gap Penalty: .05
Delay Divergent: 30
Gap Separation Distance: 8
End Gap Separation: false
Residue Specific Penalties: false
Hydrophilic Penalties: false
Hydrophilic Residues: GPSNDQEKR

	G3456	Weigel
G3456	100.0	52.3
Weigel	52.3	100.0

Since Bevan's C71448 and Wiegel's sequence show percentage identities of 52.8 and 52.3, these sequences are not encompassed by the instant claims. Applicants thus submit that Bevan, Fourgoux-Nicol, and Wiegel do not, individually or in combination, teach or suggest a transgenic plant or a method of producing a transgenic plant, as instantly claimed.

Accordingly, Applicants respectfully request that this rejection be withdrawn.

CONCLUSION

Other than the Request for Continued Examination and a request for an extension of time, Applicants believe that no additional fee is due with this communication. However, if the USPTO determines that a fee is due, the Commissioner is hereby authorized to charge Mendel Biotechnology, Inc. Deposit Account No. **50-1025**.

Respectfully submitted,
MENDEL BIOTECHNOLOGY, INC.



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